(handwritten top left) K-. Kerr

(handwritten top right) #

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *(handwritten)* 09/710,2020

Source: *(handwritten)*

Date Processed by STIC: *(handwritten)* 10/21/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) *(handwritten)* Please Note
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

(handwritten right) Please Note

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
             Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/710,2620

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

1600

```
RAW SEQUENCE LISTING              DATE: 10/21/2002
PATENT APPLICATION:  US/09/710,262D    TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw
```

```
 1 <110> APPLICANT: Rosenberg, Eugene
 2        Ron, Eliora
 3        Orr, Elisha
 4        Paitan, Yossi
 5 <120> TITLE OF INVENTION: GENE CLUSTER
 6 <130> FILE REFERENCE: 2290.00101
 7 <140> CURRENT APPLICATION NUMBER: US/09/710,262D
 8 <141> CURRENT FILING DATE: 2000-11-10
 9 <160> NUMBER OF SEQ ID NOS: 20
10 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does Not Comply Corrected Diskette Needed

pp. 1-24 errors on each page

ERRORED SEQUENCES

```
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 2392
14 <212> TYPE: Amino acid
15 <213> ORGANISM: Myxococcus xanthus
16 <400> SEQUENCE: 1
17       Val Asp Pro Ala Arg Leu Thr Arg Ala Trp Glu Gly Leu Leu Glu Arg
18        1               5                   10                  15
19       Tyr Pro Leu Leu Ala Gly Ala Ile Arg Val Glu Gly Thr Glu Pro Val
20                       20                  25                  30
21       Ile Val Pro Ser Gly Gln Val Ser Ala Glu Val His Glu Val Pro Ser
22                       35                  40                  45
23       Val Ser Asp Ser Ala Leu Val Ala Thr Leu Arg Ala Ser Ala Lys Val
24            50                  55                  60
25       Pro Phe Asp Leu Ala Cys Gly Pro Leu Ala Arg Leu His Leu Tyr Ser
26        65                  70                  75                  80
27       Arg Ser Glu His Glu His Val Leu Leu Leu Cys Phe His His Leu Val
28                       85                  90                  95
29       Leu Asp Gly Ala Ser Val Ala Pro Leu Leu Asp Ala Leu Arg Glu Arg
30                       100                 105                 110
31       Tyr Ala Gly Thr Glu Ala Lys Ala Gly Leu Leu Glu Val Pro Ile Val
32                       115                 120                 125
33       Ala Pro Tyr Arg Ala Ala Val Glu Trp Glu Gln Leu Ala Ile Gly Gly
34            130                 135                 140
35       Asp Glu Gly Arg Arg His Leu Asp Tyr Trp Arg His Val Leu Ala Thr
36            145                 150                 155                 160
37       Pro Val Pro Pro Pro Leu Asn Leu Pro Thr Asp Arg Pro Arg Ser Ala
38                       165                 170                 175
39       Thr Gly Leu Asp Ser Glu Gly Ala Thr His Ser Gln Arg Val Pro Thr
40                       180                 185                 190
```

PRT, per 1.823 of Sequence Rules

(global errors) → misaligned amino acid nos.

(see item 3 on Error Summary Sheet)

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
41   Glu Gln Ala Leu Arg Leu Arg Glu Phe Ala Arg Ala Gln Gln Val Ser
42         195             200             205
43   Leu Pro Thr Val Leu Leu Gly Leu Tyr Tyr Ala Leu Leu His Arg His
44      210             215             220
45   Thr Arg Gln Asp Asp Val Val Val Gly Ile Pro Thr Met Gly Arg Pro
46      225             230             235             240
47   Arg Ala Glu Leu Ala Thr Ala Ile Gly Tyr Phe Val Asn Val Met Ala
48             245             250             255
49   Val Arg Ala Arg Gly Leu Gly Gln His Ser Phe Gly Ser Leu Leu Arg
50         260             265             270
51   His Leu His Asp Ser Val Ile Asp Gly Leu Glu His Ala His Tyr Pro
52         275             280             285
53   Phe Pro Arg Val Val Lys Asp Leu Arg Leu Ser Asn Gly Pro Glu Glu
54      290             295             300
55   Ala Pro Gly Phe Gln Thr Met Phe Thr Phe Gln Ser Leu Gln Leu Thr
56   305             310             315             320
57   Ser Ala Pro Pro Arg Pro Glu Pro Arg Ser Gly Gly Leu Pro Glu Leu
58             325             330             335
59   Glu Pro Leu Asp Cys Val His Gln Glu Gly Ala Tyr Pro Leu Glu Leu
60         340             345             350
61   Glu Val Val Glu Gly Ala Lys Gly Leu Thr Leu His Phe Lys Tyr Asp
62         355             360             365
63   Ala Arg Leu Tyr Glu Ala Asp Thr Val Glu Arg Met Ala Arg Gln Leu
64      370             375             380
65   Leu Arg Ala Ala Asp Gln Val Ala Asp Gly Val Glu Ser Pro Leu Ser
66   385             390             395             400
67   Ala Leu Ser Trp Leu Asp Asp Glu Glu Arg Arg Thr Leu Leu Arg Asp
68             405             410             415
69   Trp Asn Ala Thr Ala Thr Pro Phe Leu Glu Asp Leu Gly Val His Glu
70             420             425             430
71   Leu Phe Gln Arg Gln Ala Arg Glu Thr Pro Asp Ala Met Ala Val Ser
72         435             440             445
73   Tyr Glu Gly His Ser Leu Ser Tyr Gln Ala Leu Asp Thr Arg Ser Arg
74      450             455             460
75   Glu Ile Ala Ala His Leu Lys Ser Phe Gly Val Lys Pro Gly Ala Leu
76   465             470             475             480
77   Val Gly Ile Tyr Leu Asp Arg Ser Ala Glu Leu Val Ala Ala Met Leu
78             485             490             495
79   Gly Val Leu Ser Ala Gly Ala Ala Tyr Val Pro Leu Asp Pro Val His
80             500             505             510
81   Pro Glu Asp Arg Leu Arg Tyr Met Leu Glu Asp Ser Gly Val Val Val
82         515             520             525
83   Val Leu Ala Arg Gln Ala Ser Arg Asp Lys Val Ala Ala Ile Ala Gly
84      530             535             540
85   Ala Ser Cys Lys Val Cys Val Leu Glu Asp Val Lys Ala Gly Ala Thr
86   545             550             555             560
87   Ser Ala Pro Ala Gly Thr Ser Pro Asn Gly Leu Ala Tyr Val Ile Tyr
88             565             570             575
89   Thr Ser Gly Ser Thr Gly Arg Pro Lys Gly Val Met Ile Pro His Arg
```

Same error

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
 90                  580              585              590
 91     Gly Val Val Asn Phe Leu Leu Cys Met Arg Arg Thr Leu Gly Leu Lys
 92          595              600              605
 93     Arg Thr Asp Ser Leu Leu Ala Val Thr Thr Tyr Cys Phe Asp Ile Ala
 94        610              615              620
 95     Ala Leu Glu Leu Leu Leu Pro Leu Cys Ala Gly Ala Gln Val Ile Ile
 96     625              630              635              640
 97     Ala Ser Ala Glu Thr Val Arg Asp Ala Gln Ala Leu Lys Arg Ala Leu
 98               645              650              655
 99     Arg Thr His Arg Pro Thr Leu Met Gln Ala Thr Pro Ala Thr Trp Thr
100               660              665              670
101      Leu Leu Phe Gln Ser Gly Trp Glu Asn Ala Glu Arg Val Arg Ile Leu
102           675              680              685
103      Cys Gly Gly Glu Ala Leu Pro Glu Ser Leu Lys Ala His Phe Val Arg
104        690              695              700
105      Thr Ala Ser Asp Val Trp Asn Met Phe Gly Pro Thr Glu Thr Thr Ile
106      705              710              715              720
107      Trp Ser Thr Met Ala Lys Val Ser Ala Ser Arg Pro Val Thr Ile Gly
108               725              730              735
109      Lys Pro Ile Asp Asn Thr Gln Val Tyr Val Leu Asp Asp Arg Met Gln
110           740              745              750
111      Pro Val Pro Ile Gly Val Pro Gly Glu Leu Trp Ile Ala Gly Ala Gly
112           755              760              765
113      Val Ala Cys Gly Tyr Leu Asn Arg Pro Ala Leu Thr Ala Glu Arg Phe
114        770              775              780
115      Val Ser Asn Pro Phe Thr Pro Gly Thr Thr Leu Tyr Arg Thr Gly Asp
116      785              790              795              800
117      Leu Ala Arg Trp Arg Ala Asp Gly Glu Val Glu Tyr Leu Gly Arg Leu
118               805              810              815
119      Asp His Gln Val Lys Val Arg Gly Phe Arg Ile Glu Met Gly Glu Ile
120           820              825              830
121      Glu Ala Gln Leu Ala Gly His Pro Ser Val Lys Asn Cys Ala Val Val
122           835              840              845
123      Ala Lys Glu Leu Asn Gly Thr Ser Gln Leu Val Ala Tyr Cys Gln Pro
124        850              855              860
125      Ala Gly Thr Ser Phe Asp Glu Glu Ala Ile Arg Ala His Leu Arg Lys
126      865              870              875              880
127      Phe Leu Pro Asp Tyr Met Val Pro Ala His Val Phe Ala Val Asp Ala
128               885              890              895
129      Ile Pro Leu Ser Gly Asn Gly Lys Val Asp Arg Gly Gln Leu Met Ala
130           900              905              910
131      Arg Pro Val Val Thr Arg Arg Lys Thr Ser Ala Val His Ala Arg Ser
132           915              920              925
133      Pro Val Glu Ala Thr Leu Val Glu Leu Trp Lys Asn Val Leu Gln Val
134        930              935              940
135      Asn Glu Val Gly Val Glu Asp Arg Phe Phe Glu Val Gly Gly Asp Ser
136      945              950              955              960
137      Val Leu Ala Ala Val Leu Val Glu Glu Met Asn Arg Arg Phe Asp Thr
138               965              970              975
```

oname

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
139    Arg Leu Ala Val Thr Asp Leu Phe Lys Tyr Val Asn Ile Arg Asp Met
140              980             985             990
141    Ala Arg His Met Glu Gly Ala Thr Ala Gln Ala Arg Thr Gly Ala Thr
142             995            1000            1005
143    Glu Pro Ala Arg Glu Asp Thr Ala Ser Glu Arg Asp Tyr Glu Gly Ser
144         1010            1015            1020
145    Leu Ala Val Ile Gly Ile Ser Cys Gln Leu Pro Gly Ala Ala Asp Pro
146       1025            1030            1035            1040
147    Trp Arg Phe Trp Lys Asn Leu Arg Glu Gly Arg Asp Ser Val Val Ala
148             1045            1050            1055
149    Tyr Arg His Glu Glu Leu Arg Glu Leu Gly Val Pro Glu Glu Val Leu
150             1060            1065            1070
151    Arg Asp Ser Arg Tyr Val Ala Val Arg Ser Ser Ile Glu Asp Lys Glu
152          1075            1080            1085
153    Cys Phe Asp Pro His Phe Phe Gly Leu Thr Ala Arg Asp Ala Ser Phe
154       1090            1095            1100
155    Met Asp Pro Gln Phe Arg Leu Leu Leu Met His Ala Trp Lys Ala Val
156    1105            1110            1115            1120
157    Glu Asp Ala Ala Thr Thr Pro Glu Arg Leu Gly Pro Cys Gly Val Phe
158             1125            1130            1135
159    Met Thr Ala Ser Asn Ser Phe Tyr His Gln Gly Ser Pro Gln Phe Pro
160             1140            1145            1150
161    Ala Asp Gly Gln Pro Val Leu Arg Thr Ala Glu Glu Tyr Val Leu Trp
162          1155            1160            1165
163    Val Leu Ala Gln Ala Gly Ser Ile Pro Thr Met Val Ser Tyr Lys Leu
164       1170            1175            1180
165    Gly Leu Lys Gly Pro Ser Leu Phe Val His Thr Asn Cys Ser Ser Ser
166    1185            1190            1195            1200
167    Leu Ser Ala Leu Tyr Val Ala Gln Gln Ala Ile Ala Ala Gly Asp Cys
168             1205            1210            1215
169    Gln Thr Ala Leu Val Gly Ala Ala Thr Val Phe Pro Ser Ala Asn Leu
170             1220            1225            1230
171    Gly Tyr Leu His Gln Arg Gly Leu Asn Phe Ser Ser Ala Gly Arg Val
172       1235            1240            1245
173    Lys Ala Phe Asp Ala Ala Ala Asp Gly Met Ile Ala Gly Glu Gly Val
174       1250            1255            1260
175    Ala Val Leu Val Val Lys Asp Ala Ala Ala Ala Val Arg Asp Gly Asp
176    1265            1270            1275            1280
177    Pro Ile Tyr Cys Leu Val Arg Lys Val Gly Ile Asn Asn Asp Gly Gln
178          1285            1290            1295
179    Asp Lys Val Gly Leu Tyr Ala Pro Ser Ala Thr Gly Gln Ala Glu Val
180             1300            1305            1310
181    Ile Arg Arg Leu Phe Asp Arg Thr Gly Ile Asp Pro Ala Ser Ile Gly
182       1315            1320            1325
183    Tyr Val Glu Ala His Gly Thr Gly Thr Leu Leu Gly Asp Pro Val Glu
184       1330            1335            1340
185    Val Ser Ala Leu Ser Glu Ala Phe Arg Thr Phe Thr Asp Arg Arg Gly
186    1345            1350            1355            1360
187    Tyr Cys Arg Leu Gly Ser Val Lys Ser Asn Leu Gly His Leu Asp Thr
```

same

1) always show one space between last amino acid number and next amino acid

e.g. Ala 1080 [space] Val

```
188                  1365              1370                1375
189     Val Ala Gly Leu Ala Gly Leu Ile Lys Thr Ala Leu Ser Leu Arg Gln
190                  1380              1385              1390
191     Gly Glu Val Pro Pro Thr Leu His Val Thr Gln Val Asn Pro Lys Leu
192                1395            1400              1405
193     Glu Leu Thr Asp Ser Pro Phe Val Ile Ala Asp Arg Leu Ala Pro Trp
194              1410              1415            1420
195     Pro Ser Leu Pro Gly Pro Arg Arg Ala Ala Val Ser Ala Phe Gly Leu
196     1425          1430            1435            1440
197     Gly Gly Thr Asn Thr His Ala Ile Leu Glu His Tyr Pro Arg Asp Ser
198                1445              1450            1455
199     Arg Pro Arg Glu Arg Ser Gln Arg Ser Asn Ala Val Arg Ala Val Ala
200              1460              1465              1470
201     Pro Phe Ser Ala Arg Thr Leu Glu Ala Leu Lys Asp Asn Leu Arg Ala
202            1475            1480            1485
203     Leu Leu Asp Phe Leu Glu Asp Pro Ala Ser Ala Glu Val Ala Leu Ala
204          1490            1495              1500
205     Asp Ile Thr Tyr Thr Leu Gln Val Gly Arg Val Ala Met Pro Glu Arg
206     1505          1510            1515            1520
207     Met Val Val Thr Ala Ser Thr Arg Asp Glu Leu Val Glu Gly Leu Arg
208                1525            1530            1535
209     Arg Gly Ile Ala Thr Val Gly Gly Ala His Val Gly Thr Val Val Asp
210              1540            1545            1550
211     Thr Ser Pro Ser Val Asp Ala Asp Ala Arg Ala Val Ala Glu Ala Trp
212            1555            1560            1565
213     Ala Thr Gly Asp Ser Ile Asp Trp Asp Ser Leu His Gly Asp Val Lys
214          1570            1575            1580
215     Pro Ala Arg Val Ser Leu Pro Thr Tyr Gln Phe Ala Lys Glu Arg Tyr
216     1585          1590            1595            1600
217     Gly Leu Ser Pro Ala His Ser Val Ala Asn Ser Ser Lys Thr His Pro
218                1605            1610            1615
219     Asp Ala Gly Val Pro Leu Phe Val Pro Thr Trp Gln Pro Trp Ser Glu
220              1620            1625            1630
221     Gly Ala Ser Asn Ala Ser Leu Ala Leu Arg His Leu Val Val Leu Cys
222            1635            1640            1645
223     Glu Pro Leu Asp Ala Leu Gly Ala Glu Gly Ala Ser Ala Leu Ala Ser
224          1650            1655            1660
225     Thr Leu Ala Asp Arg Arg Ile Glu Val Val Arg Thr Ser Ser Pro Ser
226     1665          1670            1675            1680
227     Ala Arg Leu Asp Ala Arg Phe Met Ala His Ala Ser Ala Val Phe Glu
228                1685            1690            1695
229     Arg Val Lys Ala Leu Leu Ser Glu Arg Leu Thr Ala Pro Val Thr Leu
230              1700            1705            1710
231     Gln Val Leu Val Pro Glu Glu Arg Asp Ala Leu Ala Leu Ser Gly Leu
232            1715            1720            1725
233     Gly Ser Leu Leu Arg Ser Val Ser Gln Glu Asn Pro Leu Val Arg Gly
234          1730            1735            1740
235     Gln Leu Ile Arg Val Gln Gly Ser Val Ser Ala Ser Ala Leu Val Asp
236     1745          1750            1755            1760
```

Same

```
237     Val Leu Val Lys Ser Ala Arg Ala Gly Asp Val Thr Asp Ser Arg Tyr
238              1765              1770              1775
239     His Ala Gly Gln Leu Ser Arg Cys Glu Trp Arg Glu Ala Arg Val Ala
240              1780              1785              1790
241     Lys Gly Asp Ala Ser Arg Phe Trp Arg Glu Asp Gly Val Tyr Val Ile
242              1795              1800              1805
243     Ser Gly Gly Thr Gly Ala Leu Ala Arg Leu Phe Val Ala Glu Ile Gly
244          1810              1815              1820
245     Lys Arg Ala Thr Arg Ala Thr Val Ile Leu Val Ala Arg Ala Ser Ser
246     1825              1830              1835              1840
247     Ala Glu Ala Val Asp Gly Gly Asn Gly Leu Arg Val Arg His Leu Pro
248              1845              1850              1855
249     Val Asp Val Thr Gln Pro Asn Asp Val Asn Ala Phe Val Ala Thr Val
250              1860              1865              1870
251     Leu Arg Glu His Gly Arg Ile Asp Gly Val Ile His Ala Ala Gly Ile
252          1875              1880              1885
253     Arg Arg Asp Asn Tyr Leu Leu Asn Lys Pro Val Ala Glu Met Gln Ala
254          1890              1895              1900
255     Val Leu Ala Pro Lys Val Val Gly Leu Val Asn Leu Asp His Ala Thr
256     1905              1910              1915              1920
257     Arg Glu Leu Pro Leu Asp Phe Phe Val Thr Phe Ser Ser Leu Ala Ala
258              1925              1930              1935
259     Phe Gly Asn Ala Gly Gln Ser Asp Tyr Ala Ala Ala Asn Gly Phe Met
260              1940              1945              1950
261     Asp Gly Phe Ala Glu Ser Arg Ala Ala Leu Val Asn Ala Gly Gln Arg
262          1955              1960              1965
263     Gln Gly Arg Thr Val Ser Ile Arg Trp Pro Leu Trp Glu Asn Gly Gly
264          1970              1975              1980
265     Met Gln Leu Asp Ser Arg Ser Arg Glu Val Leu Met Gln Arg Thr Gly
266     1985              1990              1995              2000
267     Met Ala Ala Leu Gly Asp Glu Ala Gly Leu Gly Ala Phe Tyr Arg Ala
268              2005              2010              2015
269     Leu Glu Leu Gly Ser Pro Gly Val Ala Val Trp Thr Gly Glu Ala Gln
270              2020              2025              2030
271     Arg Phe Arg Glu Leu Ser Val Ser Val Ser Pro Ala Pro Pro His
272          2035              2040              2045
273     Gln Val Ala Leu Asp Ala Val Val Ser Ile Thr Glu Lys Val Glu Thr
274     2050              2055              2060
275     Lys Leu Lys Ala Leu Phe Ser Glu Val Thr Arg Tyr Glu Glu Arg Arg
276     2065              2070              2075              2080
277     Ile Asp Ala Arg Gln Pro Met Glu Arg Tyr Gly Ile Asp Ser Ile Ile
278              2085              2090              2095
279     Ile Thr Gln Met Asn Gln Ala Leu Glu Gly Pro Tyr Asn Ala Leu Ser
280              2100              2105              2110
281     Lys Thr Leu Phe Phe Glu Tyr Arg Thr Leu Ala Glu Val Ser Gly Tyr
282              2115              2120              2125
283     Leu Ala Glu His Arg Ala Glu Glu Ser Ala Lys Trp Val Ala Ala Pro
284          2130              2135              2140
285     Gly Glu Asn Ser Ser Ser Val Ile Gln Glu Ala Arg Pro Pro Arg Ala
```

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
286    2145          2150          2155          2160
287    Asp Ala Thr His Arg Ala Pro Arg Ala Asp Glu Pro Ile Ala Val Ile
288              2165          2170          2175
289    Gly Met Ser Gly Arg Tyr Pro Gly Ala Glu Asn Leu Thr Glu Phe Trp
290          2180          2185          2190
291    Glu Arg Leu Ser Arg Gly Asp Asp Cys Ile Thr Glu Ile Pro Pro Glu
292        2195          2200          2205
293    Arg Trp Ser Leu Asp Gly Phe Phe Tyr Pro Asp Lys Lys His Ala Ala
294      2210          2215          2220
295    Ala Arg Gly Met Ser Tyr Ser Lys Trp Gly Gly Phe Leu Gly Gly Phe
296    2225          2230          2235          2240
297    Ala Asp Phe Asp Pro Leu Phe Phe Asn Ile Ser Pro Arg Glu Ala Thr
298          2245          2250          2255
299    Ser Met Asp Pro Gln Glu Arg Leu Phe Leu Gln Ser Cys Trp Glu Val
300          2260          2265          2270
301    Leu Glu Asp Ala Gly Tyr Thr Arg Asp Ser Leu Ala Gln Arg Phe Gly
302          2275          2280          2285
303    Ser Ala Val Gly Val Phe Ala Gly Ile Thr Lys Thr Gly Tyr Glu Leu
304      2290          2295          2300
305    Tyr Gly Ala Glu Leu Glu Gly Arg Asp Ala Ser Val Arg Pro Tyr Thr
306    2305          2310          2315          2320
307    Ser Phe Ala Ser Val Ala Asn Arg Val Ser Tyr Leu Leu Asp Leu Lys
308          2325          2330          2335
309    Gly Pro Ser Met Pro Val Asp Thr Met Cys Ser Ala Ser Leu Thr Ala
310          2340          2345          2350
311    Val His Met Ala Cys Glu Ala Leu Gln Arg Gly Ala Cys Val Met Ala
312        2355          2360          2365
313    Ile Ala Gly Gly Val Asn Leu Tyr Val His Pro Ser Ser Tyr Val Ser
314      2370          2375          2380
315    Leu Ser Gly Gln Gln Met Leu Ser
316    2385          2390
```

```
444  <210> SEQ ID NO: 3
445  <211> LENGTH: 785
446  <212> TYPE: Amino acid  PRT
447  <213> ORGANISM: Myxococcus xanthus
448  <400> SEQUENCE: 3
449    Met Lys Val Val Asn Lys Leu Leu Glu Lys Leu Pro Asp Val Val Ala
450    1           5               10              15
451    Gly Lys Val Pro Asp Val Lys Leu Gln Asp Gln Asp Ile Lys Val Pro
452              20              25              30
453    Leu Ala Gln Gly Thr Phe Thr Glu Glu Lys Ile Leu Pro Pro Lys Leu
454          35              40              45
455    Ala Met His Gly Phe Thr Leu Ser Phe Glu Ala Thr Gly Glu Ala Ser
456        50              55              60
457    Ile Arg Asn Phe Asn Ser Leu Gly Asp Val Asp Glu Asn Gly Ile Ile
458    65              70              75              80
459    Gly Glu Pro Ser Pro Glu Ser Ala Glu Pro Gly Pro Arg Pro Gln Leu
460              85              90              95
461    Leu Leu Gly Ser Asp Ile Gly Trp Met Arg Tyr Gln Val Ser Ala Arg
```

RAW SEQUENCE LISTING   DATE: 10/21/2002
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Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
462              .  100                105                110
463     Val Lys Ala Ala Val Ser Ala Ser Leu Ser Phe Leu Ala Ser Glu Asn
464            115                120                125
465     Gln Thr Glu Leu Ser Val Thr Leu Ser Asp Tyr Arg Ala His Pro Leu
466         130                135                140
467     Gly Gln Asn Met Arg Glu Ala Val Arg Ser Asp Leu Ser Glu Leu Arg
468         145                150                155                160
469     Leu Met Gln Ala Thr Asp Leu Ala Lys Leu Thr Thr Gly Asp Ala Val
470                 165         ·        170                175
471     Ala Trp His Val Arg Gly Ala Leu His Thr Arg Leu Glu Leu Asn Trp
472             180                185                190
473     Ala Asp Ile Phe Pro Thr Asn Leu Asn Arg Leu Gly Phe Leu Arg Gly
474            195                200                205
475     Asn Glu Leu Leu Ala Leu Lys Thr Ser Ala Lys Ala Gly Leu Ser Ala
476         210                215                220
477     Arg Val Ser Leu Thr Asp Asp Tyr Gln Leu Ser Phe Ser Arg Pro Arg
478     225                230                235                240
479     Ala Gly Arg Ile Gln Val Ala Val Arg Lys Val Lys Ser His Glu Gln
480                 245                250                255
481     Ala Leu Ser Ala Gly Leu Gly Ile Thr Val Glu Leu Leu Asp Pro Ala
482             260                265                270
483     Thr Val Lys Ala Gln Leu Gly Gln Leu Leu Glu Ala Leu Leu Gly Pro
484         275                280                285
485     Val Leu Arg Asp Leu Val Lys Lys Gly Thr Thr Ala Val Glu Ile Met
486         290                295                300
487     Asp Gly Leu Val Asp Lys Ala Ser Lys Ala Lys Leu Asp Asp Asn Gln
488     305                310                315                320
489     Lys Lys Val Leu Gly Leu Val Leu Glu Arg Leu Gly Ile Asp Pro Gln
490                 325                330                335
491     Leu Ala Asp Pro Ala Asn Leu Pro Gln Ala Trp Ala Asp Phe Lys Ala
492             340                345                350
493     Arg Val Ala Glu Ser Leu Glu Asn Ala Val Arg Thr Gln Val Ala Glu
494             355                360                365
495     Gly Phe Glu Tyr Glu Tyr Leu Arg Leu Ser Glu Thr Ser Thr Leu Leu
496         370                375                380
497     Glu Val Val Val Glu Asp Val Thr Ala Met Arg Phe His Glu Ser Leu
498     385                390                395                400
499     Leu Lys Gly Asn Leu Val Glu Leu Leu Lys Trp Met Lys Ser Leu Pro
500                 405                410                415
501     Ala Gln Gln Ser Glu Phe Glu Leu Arg Asn Tyr Leu His Ala Thr Thr
502             420                425                430
503     Leu Thr Arg Gln Gln Ala Ile Gly Phe Ser Leu Gly Leu Gly Ser Phe
504             435                440                445
505     Glu Leu Leu Lys Ala Lys Asn Val Ser Lys Gln Ser Trp Val Thr Gln
506         450                455                460
507     Glu Asn Phe Gln Gly Ala Arg Arg Met Ala Phe Leu Gly Arg Arg Gly
508     465                470                475                480
509     Tyr Glu Asp Lys Leu Leu Gly Thr Arg Gly Gln Trp Val Val Asp Leu
510             485                490                495
```

Same

```
511          Lys Ala Asp Met Thr Arg Phe Ser Pro Thr Pro Val Ala Ser Asp Phe
512                    500             505             510
513          Gly Tyr Gly Leu His Leu Met Leu Trp Gly Arg Gln Lys Lys Leu Ser
514               515             520             525
515          Arg Lys Asp Leu Gln Gln Ala Val Asp Asp Ala Val Val Trp Gly Val
516            530             535             540
517          Leu Asp Ala Lys Asp Ala Ala Thr Val Ile Ser Thr Met Gln Glu Asp
518          545             550             555             560
519          Met Gly Lys His Pro Ile Glu Thr Arg Leu Glu Leu Lys Met Ala Asp
520                    565             570             575
521          Asp Ser Phe Arg Ala Leu Val Pro Arg Ile Gln Thr Leu Glu Leu Ser
522                    580             585             590
523          Arg Phe Ser Arg Ala Leu Ala Arg Ala Leu Pro Trp Ser Glu Gln Leu
524               595             600             605
525          Pro Arg Ala Ser Ala Glu Phe Arg Arg Ala Val Tyr Ala Pro Ile Trp
526            610             615             620
527          Glu Ala Tyr Leu Arg Glu Val Gln Glu Gln Gly Ser Leu Met Leu Asn
528          625             630             635             640
529          Asp Leu Ser Pro Ser Arg Ala Ala Gln Ile Ala Lys Trp Tyr Phe Gln
530                    645             650             655
531          Lys Asp Pro Thr Val Arg Asp Leu Gly Lys Asp Leu Gln Leu Ile Glu
532                    660             665             670
533          Ser Glu Trp Arg Pro Gly Gly Gly Asn Phe Ser Phe Ala Glu Val Ile
534               675             680             685
535          Ser Lys Asn Pro Asn Thr Leu Met Arg Cys Arg Asn Phe Val Ser Gly
536            690             695             700
537          Met Val Arg Leu Arg Arg Ala Ile Asp Glu Arg Lys Ala Pro Asp Glu
538          705             710             715             720
539          Leu Arg Thr Val Phe Gly Glu Leu Glu Gly Met Trp Thr Thr Gly Phe
540                    725             730             735
541          His Leu Arg Ala Ala Gly Ser Leu Leu Ser Asp Leu Ala Gln Ser Thr
542               740             745             750
543          Pro Leu Gly Leu Ala Gly Val Glu Arg Thr Leu Thr Val Arg Val Ala
544               755             760             765
545          Asp Ser Glu Glu Gln Leu Val Phe Ser Thr Ala Arg Ser Thr Gly Ala
546            770             775             780
547          Ala
548          785
550 <210> SEQ ID NO: 4
551 <211> LENGTH: 529
552 <212> TYPE: Amino acid  PRT
553 <213> ORGANISM: Myxococcus xanthus
554 <400> SEQUENCE: 4
555          Met Pro Ser Gly Cys Tyr Gly Ala Ala Ser Ala Phe Val Leu Pro Pro
556            1             5             10             15
557          Leu Pro Ala Met Pro Gln Ala Pro Ser Asp Val Ser Gln Val Leu Leu
558                    20             25             30
559          Pro Phe Gly Gly Leu Val Gly Arg Glu Val Asp Leu Asp Ala Phe Leu
560                    35             40             45
```

```
561      Gln Thr Leu Met Asp Arg Ile Ala Ile Thr Leu Gln Ala Asp Arg Gly
562          50              55              60
563      Thr Leu Trp Leu Leu Asp Pro Ala Arg Arg Glu Leu Phe Ser Arg Ala
564      65              70              75              80
565      Ala His Leu Pro Glu Val Ser Gln Ile Arg Val Lys Leu Gly Gln Gly
566                  85              90              95
567      Val Ala Gly Thr Val Ala Lys Ala Gly His Ala Ile Asn Val Pro Asp
568                  100             105             110
569      Pro Arg Gly Glu Gln Arg Phe Phe Ala Asp Ile Asp Arg Met Thr Gly
570              115             120             125
571      Tyr Arg Thr Thr Ser Leu Leu Ala Val Pro Leu Arg Asp Gly Asp Gly
572          130             135             140
573      Ala Leu Tyr Gly Val Leu Gln Val Leu Asn Arg Arg Gly Glu Asp Arg
574      145             150             155             160
575      Phe Thr Asp Glu Asp Thr Gln Arg Leu Thr Ala Ile Ala Ser Gln Val
576                  165             170             175
577      Ser Thr Ala Leu Gln Ser Thr Ser Leu Tyr Gln Glu Leu Gln Arg Ala
578                  180             185             190
579      Lys Glu Gln Pro Gln Val Pro Val Gly Tyr Phe Phe Asn Arg Ile Ile
580              195             200             205
581      Gly Glu Ser Pro Gln Leu Gln Ala Ile Tyr Arg Leu Val Arg Lys Ala
582          210             215             220
583      Ala Pro Thr Asp Ala Thr Val Leu Leu Arg Gly Glu Ser Gly Ser Gly
584      225             230             235             240
585      Lys Glu Leu Phe Ala Arg Ala Val His Val Asn Gly Pro Arg Arg Asp
586                  245             250             255
587      Gln Pro Phe Ile Lys Val Asp Cys Ala Ala Leu Pro Ala Thr Leu Ile
588              260             265             270
589      Glu Asn Glu Leu Phe Gly His Glu Arg Gly Ala Phe Thr Gly Ala Asp
590              275             280             285
591      His Arg Val Pro Gly Lys Phe Glu Ala Ala Ser Gly Gly Thr Val Phe
592          290             295             300
593      Ile Asp Glu Ile Gly Glu Leu Pro Leu Pro Val Gln Gly Lys Leu Leu
594      305             310             315             320
595      Arg Val Ile Gln Asp Arg Glu Phe Glu Arg Val Gly Gly Thr Gln Ala
596              325             330             335
597      Val Lys Val Asp Val Arg Ile Val Ala Ala Thr His Arg Asp Leu Ala
598              340             345             350
599      Arg Met Val Ala Glu Gly Arg Phe Arg Glu Asp Leu Tyr Tyr Arg Ile
600          355             360             365
601      Lys Val Val Glu Val Val Leu Pro Pro Leu Arg Glu Arg Gly Ala Glu
602          370             375             380
603      Asp Ile Glu Arg Leu Ala Arg His Phe Val Ala Ala Val Ala Arg Arg
604      385             390             395             400
605      His Arg Leu Thr Pro Pro Arg Leu Ser Ala Ala Ala Val Glu Arg Leu
606              405             410             415
607      Lys Arg Tyr Arg Trp Pro Gly Asn Val Arg Glu Leu Glu Asn Cys Ile
608              420             425             430
609      Glu Ser Ala Val Val Leu Cys Glu Gly Glu Ile Leu Glu Glu His Leu
```

RAW SEQUENCE LISTING   DATE: 10/21/2002
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Input Set : **N:\Crf4\10182002\I710262D.raw**
Output Set: **N:\CRF4\10212002\I710262D.raw**

```
610                435             440             445
611       Pro Leu Pro Asp Val Asp Arg Ala Ala Leu Pro Pro Pro Ala Ala Ala
612          450             455               460
613       Gln Gly Val Asn Ala Pro Thr Ala Pro Ala Pro Leu Asp Ala Gly Leu
614       465             470             475             480
615       Leu Pro Leu Ala Glu Val Glu Arg Arg His Ile Leu Arg Val Leu Asp
616                485               490             495
617       Ala Val Lys Gly Asn Arg Thr Ala Ala Ala Arg Val Leu Ala Ile Gly
618                500             505             510
619       Arg Asn Thr Leu Ala Arg Lys Leu Lys Glu Tyr Gly Leu Gly Asp Glu
620          515             520             525
621       Pro
623  <210> SEQ ID NO: 5
624  <211> LENGTH: 292
625  <212> TYPE: Amino acid   PRT
626  <213> ORGANISM: Myxococcus xanthus
627  <400> SEQUENCE: 5
628       Met Arg Ala Ser Gln Ala Glu Ala Pro His Ser Arg Arg Leu Thr Met
629          1           5               10              15
630       Glu Val Arg Phe His Gly Val Arg Gly Ser Ile Ala Val Ser Gly Ser
631                20              25              30
632       Arg Ile Gly Gly Asn Thr Ala Cys Val Glu Val Thr Ser Gln Gly His
633          35              40              45
634       Arg Leu Ile Leu Asp Ala Gly Thr Gly Ile Arg Ala Leu Gly Glu Ile
635          50              55              60
636       Met Met Arg Glu Gly Ala Pro Gln Glu Ala Thr Leu Phe Phe Ser His
637          65              70              75              80
638       Leu His Trp Asp His Val Gln Gly Phe Pro Phe Phe Thr Pro Ala Trp
639                85              90              95
640       Leu Pro Thr Ser Glu Leu Thr Leu Tyr Gly Pro Gly Ala Asn Gly Ala
641                100             105             110
642       Gln Ala Leu Gln Ser Glu Leu Ala Ala Gln Met Gln Pro Leu His Phe
643          115             120             125
644       Pro Val Pro Leu Ser Thr Met Arg Ser Arg Met Asp Phe Arg Ser Ala
645          130             135             140
646       Leu His Ala Arg Pro Val Glu Val Gly Pro Phe Arg Val Thr Pro Ile
647       145             150             155             160
648       Asp Val Pro His Pro Gln Gly Cys Leu Ala Tyr Arg Leu Glu Ala Asp
649                165             170             175
650       Gly His Ser Phe Val Tyr Ala Thr Asp Val Glu Val Arg Val Gln Glu
651                180             185             190
652       Leu Ala Pro Glu Val Gly Arg Leu Phe Glu Gly Ala Asp Val Leu Cys
653          195             200             205
654       Leu Asp Ala Gln Tyr Thr Pro Asp Glu Tyr Glu Gly Arg Lys Gly Val
655          210             215             220
656       Ala Lys Lys Gly Trp Gly His Ser Thr Met Met Asp Ala Ala Gly Val
657       225             230             235             240
658       Ala Gly Leu Val Gly Ala Arg Arg Leu Cys Leu Phe His His Asp Pro
659                245             250             255
```

Save

```
660        Ala His Gly Asp Asp Met Leu Glu Asp Met Ala Glu Gln Ala Arg Ala
661                260                 265                 270  .
662        Leu Phe Pro Val Cys Glu Pro Ala Arg Glu Gly Gln Arg Leu Val Leu
663                275                 280                 285
664        Gly Arg Ala Ala
665                290
667 <210> SEQ ID NO: 6
668 <211> LENGTH: 168
669 <212> TYPE: Amino acid
670 <213> ORGANISM: Myxococcus xanthus
671 <400> SEQUENCE: 6
672        Met Pro Gly Pro Arg Cys Ala Glu Asn Asp Trp Val Ala Leu Leu Val
673         1               5                 10                  15
674        Arg Val Asn His Glu Lys Val Ala Ala Ala Gln Leu Gly Lys His Gly
675                20                  25                  30
676        Tyr Glu Phe Phe Leu Pro Thr Tyr Thr Pro Pro Lys Ser Ser Gly Val
677                35                  40                  45
678        Lys Ala Lys Leu Pro Leu Phe Pro Gly Tyr Leu Phe Cys Arg Tyr Gln
679                50                  55                  60
680        Pro Leu Asn Pro Tyr Arg Ile Val Arg Ala Pro Gly Val Ile Arg Leu
681         65                  70                  75                  80
682        Leu Gly Gly Asp Ala Gly Pro Glu Ala Val Pro Ala Gln Glu Leu Glu
683                        85                  90                  95
684        Ala Ile Arg Arg Val Ala Asp Ser Gly Val Ser Ser Asn Pro Cys Asp
685                100                 105                 110
686        Tyr Leu Arg Val Gly Gln Arg Val Arg Ile Ile Glu Gly Pro Leu Thr
687                115                 120                 125
688        Gly Leu Glu Gly Ser Leu Val Thr Ser Lys Ser Gln Leu Arg Phe Ile
689                130                 135                 140
690        Val Ser Val Gly Leu Leu Gln Arg Ser Val Ser Val Glu Val Ser Ala
691        145                 150                 155                 160
692        Glu Gln Leu Glu Pro Ile Thr Asp
693                        165
695 <210> SEQ ID NO: 7
696 <211> LENGTH: 79
697 <212> TYPE: Amino acid
698 <213> ORGANISM: Myxococcus xanthus
699 <400> SEQUENCE: 7
700        Met Asp Lys Arg Ile Ile Phe Asp Ile Val Thr Ser Ser Val Arg Glu
701         1               5                 10                  15
702        Val Val Pro Glu Leu Glu Ser His Pro Phe Glu Pro Glu Asp Asp Leu
703                20                  25                  30
704        Val Gly Leu Gly Ala Asn Ser Leu Asp Arg Ala Glu Ile Val Asn Leu
705                35                  40                  45
706        Thr Leu Glu Lys Leu Ala Leu Asn Ile Pro Arg Val Glu Leu Ile Asp
707                50                  55                  60
708        Ala Lys Thr Ile Gly Gly Leu Val Asp Val Leu His Ala Arg Leu
709         65                  70                  75
711 <210> SEQ ID NO: 8
```

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Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
712  <211> LENGTH: 420
713  <212> TYPE: Amino acid
714  <213> ORGANISM: Myxococcus xanthus
715  <400> SEQUENCE: 8
716     Met Gly Pro Val Gly Ile Glu Ala Met Asn Ala Tyr Cys Gly Ile Ala
717      1           5              10             15
718     Arg Leu Asp Val Leu Gln Leu Ala Thr His Arg Gly Leu Asp Thr Ser
719              20             25             30
720     Arg Phe Ala Asn Leu Leu Met Glu Glu Lys Thr Val Pro Leu Pro Tyr
721              35             40             45
722     Glu Asp Pro Val Thr Tyr Gly Val Asn Ala Ala Arg Pro Ile Leu Asp
723          50             55             60
724     Gln Leu Thr Ala Ala Glu Arg Asp Ser Ile Glu Leu Leu Val Ala Cys
725      65             70             75             80
726     Thr Glu Ser Ser Phe Asp Phe Gly Lys Ala Met Ser Thr Tyr Leu His
727              85             90             95
728     Gln His Leu Gly Leu Ser Arg Asn Cys Arg Leu Ile Glu Leu Lys Ser
729              100            105            110
730     Ala Cys Tyr Ser Gly Val Ala Gly Leu Gln Met Ala Val Asn Phe Ile
731              115            120            125
732     Leu Ser Gly Val Ser Pro Gly Ala Lys Ala Leu Val Val Ala Ser Asp
733          130            135            140
734     Leu Ser Arg Phe Ser Ile Ala Glu Gly Gly Asp Ala Ser Thr Glu Asp
735      145            150            155            160
736     Trp Ser Phe Ala Glu Pro Ser Ser Gly Ala Gly Ala Val Ala Met Leu
737              165            170            175
738     Val Ser Asp Thr Pro Arg Val Phe Arg Val Asp Val Gly Ala Asn Gly
739              180            185            190
740     Tyr Tyr Gly Tyr Glu Val Met Asp Thr Cys Arg Pro Val Ala Asp Ser
741              195            200            205
742     Glu Ala Gly Asp Ala Asp Leu Ser Leu Leu Ser Tyr Leu Asp Cys Cys
743          210            215            220
744     Glu Asn Ala Phe Arg Glu Tyr Thr Arg Arg Val Pro Ala Ala Asn Tyr
745      225            230            235            240
746     Ala Glu Ser Phe Gly Tyr Leu Ala Phe His Thr Pro Phe Gly Gly Met
747              245            250            255
748     Val Lys Gly Ala His Arg Thr Met Met Arg Lys Phe Ser Gly Lys Asn
749              260            265            270
750     Arg Gly Asp Ile Glu Ala Asp Phe Gln Arg Arg Val Ala Pro Gly Leu
751              275            280            285
752     Thr Tyr Cys Gln Arg Val Gly Asn Ile Met Gly Ala Thr Met Ala Leu
753          290            295            300
754     Ser Leu Leu Gly Thr Ile Asp His Gly Asp Phe Ala Thr Ala Lys Arg
755      305            310            315            320
756     Ile Gly Cys Phe Ser Tyr Gly Ser Gly Cys Ser Ser Glu Phe Phe Ser
757              325            330            335
758     Gly Val Val Thr Glu Glu Gly Gln Gln Arg Gln Arg Ala Leu Gly Leu
759              340            345            350
760     Gly Glu Ala Leu Gly Arg Arg Gln Gln Leu Ser Met Pro Asp Tyr Asp
```

```
        RAW SEQUENCE LISTING              DATE: 10/21/2002
        PATENT APPLICATION:  US/09/710,262D    TIME: 16:29:22

        Input Set : N:\Crf4\10182002\I710262D.raw
        Output Set: N:\CRF4\10212002\I710262D.raw
```

```
761              355              360              365
762       Ala Leu Leu Lys Gly Asn Gly Leu Val Arg Phe Gly Thr Arg Asn Ala
763          370              375              380
764       Glu Leu Asp Phe Gly Val Val Gly Ser Ile Arg Pro Gly Gly Trp Gly
765       385          390              395              400
766       Arg Pro Leu Leu Phe Leu Ser Ala Ile Arg Asp Phe His Arg Asp Tyr
767                 405              410              415
768       Gln Trp Ile Ser
769                 420
771  <210> SEQ ID NO: 9
772  <211> LENGTH: 325
773  <212> TYPE: Amino acid
774  <213> ORGANISM: Myxococcus xanthus
775  <400> SEQUENCE: 9
776       Met Ser Ser Val Ala Thr Ala Val Pro Leu Thr Ala Arg Asp Ser Ala
777        1            5              10              15
778       Val Ser Arg Arg Leu Arg Ile Thr Pro Ser Met Cys Gly Gln Thr Ser
779                 20              25              30
780       Leu Phe Ala Gly Gln Ile Gly Asp Trp Ala Trp Asp Thr Val Ser Arg
781                 35              40              45
782       Leu Cys Gly Thr Asp Val Leu Thr Ala Thr Asn Ala Ser Gly Ala Pro
783          50              55              60
784       Thr Tyr Leu Ala Phe Tyr Tyr Phe Arg Ile Arg Gly Thr Pro Ala Leu
785       65              70              75              80
786       His Pro Gly Ala Leu Arg Phe Gly Asp Thr Leu Asp Val Thr Ser Lys
787                 85              90              95
788       Ala Tyr Asn Phe Gly Ser Glu Ser Val Leu Thr Val His Arg Ile Cys
789                 100             105             110
790       Lys Thr Ala Glu Gly Gly Ala Pro Glu Ala Asp Ala Phe Gly His Glu
791          115             120             125
792       Glu Leu Tyr Glu Gln Pro Gln Pro Gly Arg Ile Tyr Ala Glu Thr Phe
793          130             135             140
794       Asn Arg Trp Ile Thr Arg Ser Asp Gly Lys Ser Asn Glu Ser Leu Ile
795       145             150             155             160
796       Lys Ser Ser Pro Val Gly Phe Gln Tyr Ala His Leu Pro Leu Leu Pro
797                 165             170             175
798       Asp Glu Tyr Ser Pro Arg Arg Ala Tyr Gly Asp Ala Arg Ala Arg Gly
799                 180             185             190
800       Thr Phe His Asp Val Asp Ser Ala Glu Tyr Arg Leu Thr Val Asp Arg
801          195             200             205
802       Phe Pro Leu Arg Tyr Ala Val Asp Val Ile Arg Asp Val Asn Gly Val
803          210             215             220
804       Gly Leu Ile Tyr Phe Ala Ser Tyr Phe Ser Met Val Asp Trp Ala Ile
805       225             230             235             240
806       Trp Gln Leu Ala Arg His Gln Gly Arg Ser Glu Gln Ala Phe Leu Ser
807                 245             250             255
808       Arg Val Val Leu Asp Gln Gln Leu Cys Phe Leu Gly Asn Ala Ala Leu
809                 260             265             270
810       Asp Thr Thr Phe Asp Ile Asp Val Gln His Trp Glu Arg Val Gly Gly
```

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
811              275           280           285
812        Gly Glu Glu Leu Phe Asn Val Lys Met Arg Glu Gly Ala Gln Gly Arg
813            290           295           300
814        Asp Ile Ala Val Ala Thr Val Lys Val Arg Phe Asp Ala Ala Ser Glu
815            305       310           315           320
816        Gly Gly Arg Arg Gly
817                  325
819 <210> SEQ ID NO: 10
820 <211> LENGTH: 83
821 <212> TYPE: Amino acid
822 <213> ORGANISM: Myxococcus xanthus
823 <400> SEQUENCE: 10
824        Met Thr Asp Glu Gln Ile Arg Gly Val Val His Gln Ser Ile Val Arg
825         1           5           10           15
826        Val Leu Pro Arg Val Arg Ser Asn Glu Ile Ala Gly His Leu Asn Leu
827                  20           25           30
828        Arg Glu Leu Gly Ala Asp Ser Val Asp Arg Val Glu Ile Leu Thr Ser
829              35           40           45
830        Ile Leu Asp Ser Leu Arg Leu Gln Lys Thr Pro Leu Ala Lys Phe Ala
831            50           55           60
832        Asp Ile Arg Asn Ile Asp Ala Leu Val Ala Phe Leu Ala Gly Glu Val
833            65           70           75           80
834        Ala Gly Gly
836 <210> SEQ ID NO: 11
837 <211> LENGTH: 374
838 <212> TYPE: Amino acid
839 <213> ORGANISM: Myxococcus xanthus
840 <400> SEQUENCE: 11
841        Met Met Gln Glu Arg Gly Val Ala Leu Pro Phe Glu Asp Pro Val Thr
842         1           5           10           15
843        Asn Ala Val Asn Ala Ala Arg Pro Ile Leu Asp Ala Met Ser Pro Glu
844                  20           25           30
845        Ala Arg Glu Arg Ile Glu Leu Leu Val Thr Ser Ser Glu Ser Gly Val
846              35           40           45
847        Asp Phe Ser Lys Ser Ile Ser Ser Tyr Ala His Glu His Leu Gly Leu
848            50           55           60
849        Ser Arg His Cys Arg Phe Leu Glu Val Lys Gln Ala Cys Tyr Ala Ala
850            65           70           75           80
851        Thr Gly Ala Leu Gln Leu Ala Leu Gly Tyr Ile Ala Ser Gly Val Ser
852                  85           90           95
853        Pro Gly Ala Lys Ala Leu Val Ile Ala Thr Asp Val Thr Leu Val Asp
854               100           105           110
855        Glu Ser Gly Leu Tyr Ser Glu Pro Ala Met Gly Thr Gly Gly Val Ala
856            115           120           125
857        Val Leu Leu Gly Asp Glu Pro Arg Val Met Lys Met Asp Leu Gly Ala
858            130           135           140
859        Phe Gly Asn Tyr Ser Tyr Asp Val Phe Asp Thr Ala Arg Pro Ser Pro
860        145           150           155           160
861        Glu Ile Asp Ile Gly Asp Val Asp Arg Ser Leu Phe Thr Tyr Leu Asp
```

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
862                  165              170              175
863     Cys Leu Lys His Ser Phe Ala Ala Tyr Gly Arg Arg Val Asp Gly Val
864          180              185              190
865     Asp Phe Val Ser Thr Phe Asp Tyr Leu Ala Met His Thr Pro Phe Ala
866          195              200              205
867     Gly Leu Val Lys Ala Gly His Arg Lys Met Met Arg Glu Leu Thr Pro
868        210              215              220
869     Cys Asp Val Asp Glu Ile Glu Ala Asp Phe Gly Arg Arg Val Lys Pro
870     225              230              235              240
871     Ser Leu Gln Tyr Pro Ser Leu Val Gly Asn Leu Cys Ser Gly Ser Val
872              245              250              255
873     Tyr Leu Ser Leu Cys Ser Ile Ile Asp Thr Ile Lys Pro Glu Arg Ser
874              260              265              270
875     Ala Arg Val Gly Met Phe Ser Tyr Gly Ser Gly Cys Ser Ser Glu Phe
876              275              280              285
877     Phe Ser Gly Val Ile Gly Pro Glu Ser Val Ser Ala Leu Ala Gly Leu
878          290              295              300
879     Asp Ile Gly Gly His Leu Arg Gly Arg Arg Gln Leu Thr Phe Asp Gln
880     305              310              315              320
881     Tyr Val Glu Leu Leu Lys Glu Asn Leu Arg Cys Leu Val Pro Thr Lys
882              325              330              335
883     Asn Arg Asp Val Asp Val Glu Arg Tyr Leu Pro Leu Val Thr Arg Thr
884              340              345              350
885     Ala Ser Arg Pro Arg Met Leu Ala Leu Arg Arg Val Val Asp Tyr His
886              355              360              365
887     Arg Gln Tyr Glu Trp Val
888          370
890  <210> SEQ ID NO: 12
891  <211> LENGTH: 171
892  <212> TYPE: Amino acid
893  <213> ORGANISM: Myxococcus xanthus
894  <400> SEQUENCE: 12
895     Met Asn Thr Pro Ser Leu Thr Asn Trp Pro Ala Arg Leu Gly Tyr Leu
896      1           5              10              15
897     Leu Ala Val Gly Gly Ala Trp Phe Ala Ala Asp Gln Val Thr Lys Gln
898              20              25              30
899     Met Ala Arg Asp Gly Ala Lys Arg Pro Val Ala Val Phe Asp Ser Trp
900          35              40              45
901     Trp His Phe His Tyr Val Glu Asn Arg Ala Gly Ala Phe Gly Leu Phe
902          50              55              60
903     Ser Ser Phe Gly Glu Glu Trp Arg Met Pro Phe Phe Tyr Val Val Gly
904     65              70              75              80
905     Ala Ile Cys Ile Val Leu Leu Ile Gly Tyr Tyr Phe Tyr Thr Pro Pro
906              85              90              95
907     Thr Met Lys Leu Gln Arg Trp Ser Leu Ala Thr Met Ile Gly Gly Ala
908              100             105             110
909     Leu Gly Asn Tyr Val Asp Arg Val Arg Leu Arg Tyr Val Val Asp Phe
910          115             120             125
911     Val Ser Trp His Val Gly Asp Arg Phe Tyr Trp Pro Ser Phe Asn Ile
```

same

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
912          130              135              140
913     Ala Asp Thr Ala Val Val Val Gly Ala Ala Leu Met Ile Leu Glu Ser
914     145          150              155              160
915     Phe Arg Glu Pro Arg Gln Gln Leu Ser Pro Gly
916·                 165              170
918  <210> SEQ ID NO: 13
919  <211> LENGTH: 475
920  <212> TYPE Amino acid
921  <213> ORGANISM: Myxococcus xanthus
922  <400> SEQUENCE: 13
923     Met Gly Thr Ser Glu Pro Val Glu Pro Asp His Ala Leu Ser Lys Pro
924      1           5                10               15
925     Pro Pro Val Ala Pro Val Gly Ala Gln Ala Leu Pro Arg Gly Pro Ala
926                  20               25               30
927     Met Pro Gly Ile Ala Gln Leu Met Met Leu Phe Leu Arg Pro Thr Glu
928          35               40               45
929     Phe Leu Asp Arg Cys Ala Ala Arg Tyr Gly Asp Thr Phe Thr Leu Lys
930          50               55               60
931     Ile Pro Gly Thr Pro Pro Phe Ile Gln Thr Ser Asp Pro Ala Leu Ile
932     65           70               75               80
933     Glu Val Ile Phe Lys Gly Asp Pro Asp Leu Phe Leu Gly Gly Lys Ala
934                  85               90               95
935     Asn Asn Gly Leu Lys Pro Val Val Gly Glu Asn Ser Leu Leu Val Leu
936                  100              105              110
937     Asp Gly Lys Arg His Arg Arg Asp Arg Lys Leu Ile Met Pro Thr Phe
938                  115              120              125
939     Leu Gly Glu Arg Met His Ala Tyr Gly Ser Val Ile Arg Asp Ile Val
940          130              135              140
941     Asn Ala Ala Leu Asp Arg Trp Pro Val Gly Lys Pro Phe Ala Val His
942     145              150              155              160
943     Glu Glu Thr Gln Gln Ile Met Leu Glu Val Ile Leu Arg Val Ile Phe
944                  165              170              175
945     Gly Leu Glu Asp Ala Arg Thr Ile Ala Gln Phe Arg His His Val His
946                  180              185              190
947     Gln Val Leu Lys Leu Ala Leu Phe Leu Phe Pro Asn Gly Glu Gly Lys
948                  195              200              205
949     Pro Ala Ala Glu Gly Phe Ala Arg Ala Val Gly Lys Ala Phe Pro Ser
950          210              215              220
951     Leu Asp Val Phe Ala Ser Leu Lys Ala Ile Asp Asp Ile Ile Tyr Gln
952     225              230              235              240
953     Glu Ile Gln Asp Arg Arg Ser Gln Asp Ile Ser Gly Arg Gln Asp Val
954                  245              250              255
955     Leu Ser Leu Met Met Gln Ser His Tyr Asp Asp Gly Ser Val Met Thr
956                  260              265              270
957     Pro Gln Glu Leu Arg Asp Glu Leu Met Thr Leu Leu Met Ala Gly His
958          275              280              285
959     Glu Thr Ser Ala Thr Ile Ala Ala Trp Cys Val Tyr His Leu Cys Arg
960          290              295              300
961     His Pro Asp Ala Met Gly Lys Leu Arg Glu Glu Ile Ala Ala His Thr
```

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962        305                 310                 315                 320
963        Val Asp Gly Val Leu Pro Leu Ala Lys Ile Asn Glu Leu Lys Phe Leu
964                        325                 330                 335
965        Asp Ala Val Val Lys Glu Thr Met Arg Ile Thr Pro Val Phe Ser Leu
966                    340                 345                 350
967        Val Ala Arg Val Leu Lys Glu Pro Gln Thr Ile Gly Gly Thr Thr Tyr
968                    355                 360                 365
969        Pro Ala Asn Val Val Leu Ser Pro Asn Ile Tyr Gly Thr His His Arg
970            370                 375                 380
971        Ala Asp Leu Trp Gly Asp Pro Lys Val Phe Arg Pro Glu Arg Phe Leu
972        385                 390                 395                 400
973        Glu Glu Arg Val Asn Pro Phe His Tyr Phe Pro Phe Gly Gly Gly Ile
974                        405                 410                 415
975        Arg Lys Cys Ile Gly Thr Ser Phe Ala Tyr Tyr Glu Met Lys Ile Phe
976                    420                 425                 430
977        Val Ser Glu Thr Val Arg Arg Met Arg Phe Asp Thr Arg Pro Gly Tyr
978                435                 440                 445
979        His Ala Lys Val Val Arg Arg Ser Asn Thr Leu Ala Pro Ser Gln Gly
980            450                 455                 460
981        Val Pro Ile Ile Val Glu Ser Arg Leu Pro Ser
982        465                 470                 475
984 <210>  SEQ ID NO: 14
985 <211>  LENGTH: 318
986 <212>  TYPE: Amino acid
987 <213>  ORGANISM: Myxococcus xanthus
988 <400>  SEQUENCE: 14
989        Met Val Asp Ser Val Ser Lys Gln Ala Arg Arg Lys Val Phe Leu Phe
990        1               5                   10                  15
991        Ser Gly Gln Gly Thr Gln Ser Tyr Phe Met Ala Lys Glu Leu Phe Asp
992                    20                  25                  30
993        Thr Gln Thr Gly Phe Lys Arg Gln Leu Leu Glu Leu Asp Glu Gln Phe
994                35                  40                  45
995        Lys Gln Arg Leu Gly His Ser Ile Leu Glu Arg Ile Tyr Asp Ala Arg
996            50                  55                  60
997        Ala Ala Arg Leu Asp Pro Leu Asp Asp Val Leu Val Ser Phe Pro Ala
998        65                  70                  75                  80
999        Ile Phe Met Ile Glu His Ala Leu Ala Arg Leu Leu Ile Asp Arg Gly
1000                       85                  90                  95
1001        Ile Gln Pro Asp Ala Val Val Gly Ala Ser Met Gly Glu Val Ala Ala
1002                    100                 105                 110
1003        Ala Ala Ile Ala Gly Ala Ile Ser Val Asp Ala Ala Val Ala Leu Val
1004            115                 120                 125
1005        Ala Ala Gln Ala Gln Leu Phe Ala Arg Thr Ala Pro Arg Gly Gly Met
1006            130                 135                 140
1007        Leu Ala Val Leu His Glu Leu Glu Ala Cys Arg Gly Phe Thr Ser Val
1008        145                 150                 155                 160
1009        Ala Arg Asp Gly Glu Val Ala Ala Ile Asn Tyr Pro Ser Asn Phe Val
1010                    165                 170                 175
1011        Leu Ala Ala Asp Glu Ala Gly Leu Gly Arg Ile Gln Gln Glu Leu Ser
```

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:22

Input Set : N:\Crf4\10182002\I710262D.raw
Output Set: N:\CRF4\10212002\I710262D.raw

```
1012                   180              185                   190
1013      Gln Arg Ser Val Ala Phe His Arg Leu Pro Val Arg Tyr Pro Phe His
1014               195                  200                   205
1015      Ser Ser His Leu Asp Pro Leu Arg Glu Glu Tyr Arg Ser Arg Val Arg
1016         210                  215                  220
1017      Ala Asp Ser Leu Thr Trp Pro Arg Ile Pro Met Tyr Ser Cys Thr Thr
1018         225                  230              235                 240
1019      Ala Asn Arg Val His Asp Leu Arg Ser Asp His Phe Trp Asn Val Val
1020                   245                  250                  255
1021      Arg Ala Pro Ile Gln Leu Tyr Asp Thr Val Leu Gln Leu Glu Gly Gln
1022               260                  265                  270
1023      Gly Gly Cys Asp Phe Ile Asp Val Gly Pro Ala Ala Ser Phe Ala Thr
1024               275                  280                  285
1025      Ile Ile Lys Arg Ile Leu Ala Arg Asp Ser Thr Ser Arg Leu Phe Pro
1026         290                  295                  300
1027      Leu Leu Ser Pro Ser Pro Ala Ser Thr Gly Ser Ser Met Gly
1028      305                  310                  315
1030 <210> SEQ ID NO: 15
1031 <211> LENGTH: 330
1032 <212> TYPE: Amino acid
1033 <213> ORGANISM: Myxococcus xanthus
1034 <400> SEQUENCE: 15
1035      Met Thr Glu Ala Pro Ala Pro Arg Ala Pro Ala Gln Val Pro Pro Pro
1036      1               5                   10                  15
1037      Pro Ser Ser Pro Trp Ala Leu His Thr Arg Gly Ala Ala Ser Ala Pro
1038               20                  25                   30
1039      Val Asn Ala Arg Lys Ala Ala Leu Phe Pro Gly Gln Gly Ser Gln Glu
1040               35                  40                   45
1041      Arg Gly Met Gly Ala Ala Leu Phe Asp Glu Phe Pro Asp Leu Thr Asp
1042               50                  55                   60
1043      Ile Ala Asp Ala Ile Leu Gly Tyr Ser Ile Lys Arg Leu Cys Leu Glu
1044      65                  70                   75                  80
1045      Asp Pro Gly Lys Glu Leu Ala Gln Thr Gln Phe Thr Gln Pro Ala Leu
1046                   85                  90                   95
1047      Tyr Val Val Asn Ala Leu Ser Tyr Leu Lys Arg Leu Arg Glu Gly Ala
1048               100                 105                  110
1049      Glu Gln Pro Ala Phe Val Ala Gly His Ser Leu Gly Glu Tyr Asn Ala
1050               115                 120                  125
1051      Leu Leu Val Ala Gly Ala Phe Asp Phe Glu Thr Gly Leu Arg Leu Val
1052               130                 135                  140
1053      Lys Arg Arg Gly Glu Leu Met Ser Gly Ala Ser Gly Gly Thr Met Ala
1054      145                 150                  155                 160
1055      Ala Val Val Gly Cys Asp Ala Val Ala Val Glu Gln Val Leu Arg Asp
1056               165                 170                  175
1057      Arg Gln Leu Thr Ser Leu Asp Ile Ala Asn Ile Asn Ser Pro Asp Gln
1058               180                 185                  190
1059      Ile Val Val Ser Gly Pro Ala Gln Asp Ile Glu Arg Ala Arg Gln Cys
1060               195                 200                  205
1061      Phe Val Asp Arg Gly Ala Arg Tyr Val Pro Leu Asn Val Arg Ala Pro
```

Same

RAW SEQUENCE LISTING   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:22

Input Set : **N:\Crf4\10182002\I710262D.raw**
Output Set: **N:\CRF4\10212002\I710262D.raw**

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1062         210              215              220
1063    Phe His Ser Arg Tyr Met Gln Pro Ala Ala Ser Glu Phe Glu Arg Phe
1064    225            230             235              240
1065    Leu Ser Gln Phe Gln Tyr Ala Pro Leu Arg Cys Val Val Ile Ser Asn
1066              245             250             255
1067    Val Thr Gly Arg Pro Tyr Ala His Asp Asn Val Val Gln Gly Leu Ala
1068         260             265             270
1069    Leu Gln Leu Arg Ser Pro Val Gln Trp Thr Ala Thr Val Arg Tyr Leu
1070         275             280             285
1071    Leu Glu Gln Gly Val Glu Asp Phe Glu Glu Leu Gly Pro Gly Arg Val
1072         290             295             300
1073    Leu Thr Arg Leu Ile Thr Ala Asn Lys Arg Gly Ala Pro Ala Pro Ala
1074    305            310             315              320
1075    Thr Ala Ala Pro Ala Lys Trp Ala Asn Ala
1076              325             330
1078  <210> SEQ ID NO: 16
1079  <211> LENGTH: 417
1080  <212> TYPE: Amino acid
1081  <213> ORGANISM: Myxococcus xanthus
1082  <400> SEQUENCE: 16
1083    Met Ser Thr Ser Pro Val Gln Glu Leu Val Val Ser Gly Phe Gly Val
1084    1              5               10              15
1085    Thr Ser Ala Ile Gly Gln Gly Ala Ala Ser Phe Thr Ser Ala Leu Leu
1086              20              25              30
1087    Glu Gly Ala Ala Arg Phe Arg Val Met Glu Arg Pro Gly Arg Gln His
1088         35              40              45
1089    Gln Ala Asn Gly Gln Thr Thr Ala His Leu Gly Ala Glu Ile Ala Ser
1090         50              55              60
1091    Leu Ala Val Pro Glu Gly Val Thr Pro Gln Leu Trp Arg Ser Ala Thr
1092    65             70              75              80
1093    Phe Ser Gly Gln Ala Ala Leu Val Thr Val His Glu Ala Trp Asn Ala
1094              85              90              95
1095    Ala Arg Leu Gln Ala Val Pro Gly His Arg Ile Gly Leu Val Val Gly
1096              100             105             110
1097    Gly Thr Asn Val Gln Gln Arg Asp Leu Val Leu Met Gln Asp Ala Tyr
1098         115             120             125
1099    Arg Glu Arg Val Pro Phe Leu Arg Ala Ala Tyr Gly Ser Thr Phe Met
1100         130             135             140
1101    Asp Thr Asp Leu Val Gly Leu Cys Thr Gln Gln Phe Ala Ile His Gly
1102    145            150             155             160
1103    Met Ser Phe Thr Val Gly Gly Ala Ser Ala Ser Gly Leu Leu Ala Val
1104              165             170             175
1105    Ile Gln Ala Ala Glu Ala Val Leu Ser Arg Lys Val Asp Val Cys Ile
1106         180             185             190
1107    Ala Val Gly Ala Leu Met Asp Val Ser Tyr Trp Glu Cys Gln Gly Leu
1108         195             200             205
1109    Arg Ala Met Gly Ala Met Gly Thr Asp Arg Phe Ala Arg Glu Pro Glu
1110    210            215             220
1111    Arg Ala Cys Arg Pro Phe Asp Arg Glu Ser Asp Gly Phe Ile Phe Gly
```

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1112           225              230              235              240
1113     Glu Ala Cys Gly Ala Val Val Val Glu Ser Ala Glu His Ala Arg Arg
1114              245              250              255
1115     Arg Gly Val Thr Pro Arg Gly Ile Leu Ser Gly Trp Ala Met Gln Leu
1116          260              265              270
1117     Asp Ala Ser Arg Gly Pro Leu Ser Ser Ile Glu Arg Glu Ser Gln Val
1118          275              280              285
1119     Ile Gly Ala Ala Leu Arg His Ala Asp Leu Ala Pro Glu Arg Val Asp
1120        290              295              300
1121     Tyr Val Asn Pro His Gly Ser Gly Ser Arg Gln Gly Asp Ala Ile Glu
1122     305              310              315              320
1123     Leu Gly Ala Leu Lys Ala Cys Gly Leu Thr His Ala Arg Val Asn Thr
1124              325              330              335
1125     Thr Lys Ser Ile Thr Gly His Gly Leu Ser Ser Ala Gly Ala Val Gly
1126              340              345              350
1127     Leu Ile Ala Thr Leu Val Gln Leu Glu Gln Gly Arg Leu His Pro Ser
1128          355              360              365
1129     Leu Asn Leu Val Asp Pro Ile Asp Ser Ser Phe Arg Trp Val Gly Ala
1130          370              375              380
1131     Thr Ala Glu Ala Gln Ser Leu Gln Asn Ala Leu Val Leu Ala Tyr Gly
1132     385              390              395              400
1133     Phe Gly Gly Ile Asn Thr Ala Val Ala Val Arg Arg Ser Ala Thr Glu
1134              405              410              415
1135     Ser
1137 <210> SEQ ID NO: 17
1138 <211> LENGTH: 262
1139 <212> TYPE: Amino acid
1140 <213> ORGANISM: Myxococcus xanthus
1141 <400> SEQUENCE: 17
1142     Met Gln Ala Ala Ser Pro Pro His Arg Asp Tyr Gln Thr Leu Arg Val
1143       1              5              10              15
1144     Arg Phe Glu Ala Gln Thr Cys Phe Leu Gln Leu His Arg Pro Asp Ala
1145              20              25              30
1146     Asp Asn Thr Ile Ser Arg Thr Leu Ile Asp Glu Cys Gln Gln Val Leu
1147          35              40              45
1148     Thr Leu Cys Glu Glu His Ala Thr Thr Val Val Leu Glu Gly Leu Pro
1149          50              55              60
1150     His Val Phe Cys Met Gly Ala Asp Phe Arg Ala Ile His Asp Arg Val
1151     65              70              75              80
1152     Asp Asp Gly Arg Arg Glu Gln Gly Asn Ala Glu Gln Leu Tyr Arg Leu
1153              85              90              95
1154     Trp Leu Gln Leu Ala Thr Gly Pro Tyr Val Thr Val Ala His Val Gln
1155              100             105             110
1156     Gly Lys Ala Asn Ala Gly Gly Leu Gly Phe Val Ser Ala Cys Asp Ile
1157          115             120             125
1158     Val Leu Ala Lys Ala Glu Val Gln Phe Ser Leu Ser Glu Leu Leu Phe
1159          130             135             140
1160     Gly Leu Phe Pro Ala Cys Val Met Pro Phe Leu Ala Arg Arg Ile Gly
1161     145             150             155             160
```

```
1162        Ile Gln Arg Ala His Tyr Leu Thr Leu Met Thr Arg Pro Ile Asp Ala
1163                165                 170                 175
1164        Ala Gln Ala Leu Ser Trp Gly Leu Ala Asp Ala Val Asp Ala Asp Ser
1165                180                 185                 190
1166        Glu Lys Leu Leu Arg Leu His Leu Arg Arg Leu Arg Cys Leu Ser Lys
1167                195                 200                 205
1168        Pro Ala Val Thr Gln Tyr Lys Lys Tyr Ala Ser Glu Leu Gly Gly Gln
1169            210                 215                 220
1170        Leu Leu Ala Ala Met Pro Arg Ala Ile Ser Ala Asn Glu Ala Met Phe
1171        225                 230                 235                 240
1172        Ser Asp Arg Ala Thr Leu Glu Ala Ile His Arg Tyr Val Glu Thr Gly
1173                245                 250                 255
1174        Arg Leu Pro Trp Glu Ser
1175                260
1177 <210> SEQ ID NO: 18
1178 <211> LENGTH: 256
1179 <212> TYPE: Amino acid
1180 <213> ORGANISM: Myxococcus xanthus
1181 <400> SEQUENCE: 18
1182        Met Gly Ile Met Thr Glu Gly Thr Pro Met Ala Pro Val Val Thr Leu
1183         1           5                   10                  15
1184        His Glu Val Glu Glu Gly Val Ala Gln Ile Thr Leu Val Asp Arg Glu
1185                20                  25                  30
1186        Asn Lys Asn Met Phe Ser Glu Gln Leu Val Arg Glu Leu Ile Thr Val
1187                35                  40                  45
1188        Phe Gly Lys Val Asn Gly Asn Glu Arg Tyr Arg Ala Val Val Leu Thr
1189            50                  55                  60
1190        Gly Tyr Asp Thr Tyr Phe Ala Leu Gly Gly Thr Lys Ala Gly Leu Leu
1191        65                  70                  75                  80
1192        Ser Ile Cys Asp Gly Ile Gly Ser Phe Asn Val Thr Asn Phe Tyr Ser
1193                85                  90                  95
1194        Leu Ala Leu Glu Cys Asp Ile Pro Val Ile Ser Ala Met Gln Gly His
1195                100                 105                 110
1196        Gly Val Gly Gly Gly Phe Ala Met Gly Leu Phe Ala Asp Phe Val Val
1197            115                 120                 125
1198        Leu Ser Arg Glu Ser Val Tyr Thr Thr Asn Phe Met Arg Tyr Gly Phe
1199            130                 135                 140
1200        Thr Pro Gly Met Gly Ala Thr Tyr Ile Val Pro Lys Arg Leu Gly Tyr
1201        145                 150                 155                 160
1202        Ser Leu Gly His Glu Leu Leu Leu Asn Ala Arg Asn Tyr Arg Gly Ala
1203                165                 170                 175
1204        Asp Leu Glu Lys Arg Gly Val Pro Phe Pro Val Leu Pro Arg Lys Glu
1205            180                 185                 190
1206        Val Leu Pro His Ala Tyr Glu Ile Ala Arg Asp Leu Ala Ala Lys Pro
1207            195                 200                 205
1208        Arg Leu Ser Leu Val Thr Leu Lys Arg His Leu Val Arg Asp Ile Arg
1209            210                 215                 220
1210        Arg Glu Leu Pro Asp Val Ile Glu Arg Glu Leu Glu Met His Gly Ile
1211        225                 230                 235                 240
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1212        Thr Phe His His Asp Asp Val Arg Arg Arg Ile Glu Gln Leu Phe Leu
1213                245                 250                 255
1215  <210>  SEQ ID NO: 19
1216  <211>  LENGTH: 424
1217  <212>  TYPE( Amino acid )
1218  <213>  ORGANISM: Myxococcus xanthus
1219  <400>  SEQUENCE: 19
1220        Met Leu Asn Leu Ile Asn Asn His Ala His Gly Tyr Val Val Thr Pro
1221         1               5                  10                 15
1222        Val Val Leu Ala Cys Asn Asp Ala Gly Leu Phe Glu Leu Leu Arg Gln
1223                20                  25                  30
1224        Gly Pro Lys Asp Phe Asp Arg Leu Ala Glu Ala Leu Arg Ala Asn Arg
1225                35                  40                  45
1226        Gly His Leu Arg Val Ala Met Arg Met Phe Glu Ser Leu Gly Trp Val
1227                50                  55                  60
1228        Arg Arg Asp Ala Asp Asp Val Tyr Ala Val Thr Ala Ala Ala Ala Ala
1229        65                  70                  75                  80
1230        His Arg Ser Phe Pro Arg Glu Ala Gln Ser Leu Phe Ala Leu Pro Met
1231                    85                  90                  95
1232        Asp Arg Tyr Leu Arg Gly Glu Asp Gly Leu Ser Leu Ala Pro Trp Phe
1233                    100                 105                 110
1234        Glu Arg Ser Arg Ala Ser Trp Asp Thr Asp Asp Thr Leu Val Arg Glu
1235                115                 120                 125
1236        Leu Leu Asp Gly Ala Ile Ile Thr Pro Leu Met Leu Ala Leu Glu Gln
1237            130                 135                 140
1238        Arg Gly Gly Leu Lys Glu Ala Arg Arg Leu Ser Asp Leu Trp Ser Gly
1239        145                 150                 155                 160
1240        Gly Asp Gly Arg Asp Thr Cys Val Pro Glu Ala Val Gln His Glu Leu
1241                165                 170                 175
1242        Ala Gly Phe Phe Ser Ala Gln Lys Trp Thr Arg Glu Asp Ala Val Asp
1243                180                 185                 190
1244        Ala Glu Leu Thr Pro Lys Gly Ala Phe Ile Phe Glu Arg Ala Leu Leu
1245            195                 200                 205
1246        Phe Ala Ile Val Gly Ser Tyr Arg Pro Met Leu Ala Ser Met Pro Gln
1247            210                 215                 220
1248        Leu Leu Phe Gly Asp Cys Asp Gln Val Phe Gly Arg Asp Glu Ala Gly
1249        225                 230                 235                 240
1250        His Glu Leu His Leu Asp Arg Thr Leu Asn Val Ile Gly Ser Gly His
1251                245                 250                 255
1252        Gln His Arg Lys Tyr Phe Ala Glu Leu Glu Lys Leu Ile Ile Thr Val
1253                260                 265                 270
1254        Phe Asp Ala Glu Asn Leu Ser Ala Gln Pro Arg Tyr Ile Ala Asp Met
1255                275                 280                 285
1256        Gly Cys Gly Asp Gly Thr Leu Leu Lys Arg Val Tyr Glu Thr Val Leu
1257            290                 295                 300
1258        Arg His Thr Arg Arg Gly Arg Ala Leu Asp Arg Phe Pro Leu Thr Leu
1259        305                 310                 315                 320
1260        Ile Ala Ala Asp Phe Asn Glu Lys Ala Leu Glu Ala Ala Gly Arg Thr
1261                325                 330                 335
```

```
1262      Leu Ala Gly Leu Glu His Val Ala Leu Arg Ala Asp Val Ala Arg Pro
1263              340             345             350
1264      Asp Arg Leu Ile Glu Asp Leu Arg Ala Arg Gly Leu Ala Glu Pro Glu
1265              355             360             365
1266      Asn Thr Leu His Ile Arg Ser Phe Leu Asp His Asp Arg Pro Tyr Gln
1267          370             375             380
1268      Pro Pro Ala Asp Arg Ala Gly Leu His Ala Arg Ile Pro Phe Asp Ser
1269      385             390             395             400
1270      Val Phe Val Gly Lys Ala Gly Gln Glu Val Val Pro Ala Glu Val Phe
1271              405             410             415
1272      His Ser Leu Val Glu His Leu Glu
1273              420
```

VERIFICATION SUMMARY   DATE: 10/21/2002
PATENT APPLICATION: US/09/710,262D   TIME: 16:29:23

Input Set : **N:\Crf4\10182002\I710262D.raw**
Output Set: **N:\CRF4\10212002\I710262D.raw**

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L:7 M:270 C: Current Application Number differs, Wrong Format
L:16 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:448 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:554 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:627 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:671 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:699 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:715 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:775 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:823 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:840 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:894 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:922 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:988 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1034 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1082 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1141 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1181 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:1219 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
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